The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

1.-16. (Cancelled)

17. (Currently amended) A method of identifying two or more markers useful for diagnosing a disease, said method comprising:

for each gene of a collection of two or more genes, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having said disease:

(a) using an oligonucleotide of predetermined sequence, detecting a presence, in RNA of blood samples which have not been fractionated into cell types from subjects having said disease, of RNA encoded by said gene, said oligonucleotide being specific only for RNA, or cDNA complementary to said RNA, encoded by said gene in said samples~~, said gene being expressed in blood and in a non-blood tissue of a subject not having said disease~~;

(b) quantifying a level of said RNA encoded by said gene; and

(c) determining a difference between said ~~quantified~~ level, and a quantified level of control RNA encoded by said gene in RNA of blood samples which have not been fractionated into cell types from control subjects, said control RNA having been detected in said samples from said control subjects, and said difference identifying said gene as a ~~further~~ marker of said disease,

thereby identifying said two or more markers ~~as~~ useful for diagnosing said disease.

18. (Cancelled)

19. (Currently amended) A method of identifying two or more markers useful for diagnosing a disease, said method comprising:

for each gene of a collection of two or more genes, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having said disease:

(a) producing amplification products from RNA of blood samples which have not been fractionated into cell types from subjects having said disease, using primers specific only for RNA, and/or cDNA complementary to said RNA, encoded by said gene~~, of said subjects, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having said~~

~~disease;~~

(b) quantifying a level of said amplification products; and

(c) determining a difference between said ~~quantified~~ level of said amplification products, and a quantified level of control amplification products produced from control RNA using primers specific only for said RNA, and/or cDNA complementary to said RNA, encoded by said gene ~~using said primers, from control RNA,~~ in RNA of blood samples which have not been fractionated into cell types~~,~~ from control subjects, said control ~~RNA~~ amplification products having been detected in said samples from said control subjects, wherein said difference identifies said ~~second~~ gene as a marker of said disease,

~~T~~thereby identifying said two or more markers ~~as~~ useful for diagnosing ~~the~~said disease.

20. (Currently amended) The method of any one of claims ~~1, 7 and~~ 17~~,~~ and 54, wherein said detecting of said RNA encoded by ~~each~~ said gene of step (a) is effected by detecting cDNA and/or EST derived from said RNA of step (a).

21. (Currently amended) The method of any one of claims ~~2, 8 and~~ 19~~,~~ and 55, wherein said producing of said amplification products of step (a) is effected by producing ~~an~~ amplification products from cDNA and/or EST derived from said RNA encoded by ~~each~~ said gene of step (a).

22. (Cancelled)

23. (Currently amended) The method of any one of claims ~~1, 7 and~~ 17~~,~~ and 54, further comprising quantifying said control RNA to determine said quantified level of said control RNA.

24. (Currently amended) The method of any one of claims ~~2, 8 and~~ 19~~,~~ and 55, ~~further~~ comprising quantifying a level of said control amplification products ~~from said control RNA~~ to thereby determine said quantified level of said control amplification products ~~produced from said control RNA~~.

25. (Cancelled)

26. (Cancelled)

27. (Cancelled)

28. (Currently amended) The method of any one of claims ~~1, 2, 7, 8,~~ 17 and 54, ~~and 19,~~ wherein said quantifying of said level of said RNA encoded by said gene in step (b) is effected by determining a quantity of said RNA relative to a housekeeping gene.

29 (Currently amended) The method of any one of claims ~~1, 7 and~~ 17~~,~~ and 54, wherein said quantified level of said control RNA encoded by said gene has been ~~determining~~ determined relative to a housekeeping gene.

30. (Cancelled)

31. (Currently amended) The method of any one of claims ~~2, 8 and~~ 19~~,~~ and 55, wherein said quantified level of said amplification products produced from said control RNA has been determined relative to a housekeeping gene.

32. (Cancelled)

33. (Currently amended) The method of any one of claims ~~1, 2, 7, 8,~~ 17, ~~and~~ 19, 54 and 55, wherein said control subjects and said subjects having said disease are human.

34. (Currently amended) The method of any one of claims ~~1, 2, 7 8,~~ 17, ~~and~~ 19, 54 and 55, wherein ~~none of s~~said control subjects do not have said disease.

35. (Cancelled)

36. (Cancelled)

37. (Cancelled)

38. (Currently amended) The method of any one of claims ~~2, 8 or~~ 19~~,~~ and 55, wherein said quantifying~~producing~~ of said amplification products ~~of step~~encoded by said gene in step (a~~b~~) is effected by ~~producing~~quantifying amplification products produced from cDNA and/or EST derived from said RNA of step (a).

39. (Currently amended) The method of any one of claims ~~7, 8,~~ 17~~,~~ ~~or~~ 19, 54 and 55, wherein said subjects having said disease have no overt symptoms with respect to said disease.

40. (Cancelled)

41. (Currently amended) The method of any one of claims~~1, or~~ 17 and 54~~,~~ wherein said quantifying of said level of said RNA encoded by~~each~~ said gene ~~of~~in step (a~~b~~) is effected by quantifying a level of cDNA and/or EST derived from said RNA encoded by ~~each~~ said gene ~~of step (a)~~.

42. (Cancelled)

43. (Currently amended) The method of any one of claims ~~1, 2, 7, 8,~~ 17, ~~or~~ 19, 54 and 55, wherein said disease is selected from the group consisting of colorectal cancer, diabetes, and heart failure.

44. (Cancelled)

45. (Cancelled)

46. (Currently amended) The method of any one of claims ~~7, 8,~~ 17, ~~or~~ 19, 54 and 55, wherein said subjects having said disease are asymptomatic with respect to said disease.

47. (Cancelled)

48. (Cancelled)

49. (Currently amended) The method of any one of claims ~~7, 8,~~ 17, ~~or~~ 19, 54 and 55, wherein said control subjects have said disease at a different stage than said subjects having said disease.

50. (Cancelled)

51. (Cancelled)

52. (Cancelled)

53. (Cancelled)

54. (Currently amended) A method of identifying two or more markers useful for diagnosing a disease, said method comprising:

for each gene of a collection of two or more genes, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having said disease:

(a) using an oligonucleotide of predetermined sequence, detecting a presence, in RNA of unfractionated cells of lysed blood samples from subjects having said disease, of RNA encoded by said gene, said oligonucleotide being specific only for RNA, or cDNA complementary to said RNA, encoded by said gene in said samples~~, and said gene being expressed in blood and in a non-blood tissue of a subject not having said disease~~;

(b) quantifying a level of said RNA encoded by said gene in said samples; and

(c) determining a difference between said ~~quantified~~ level, and a quantified level of control RNA encoded by said gene in RNA of unfractionated cells of lysed blood samples~~,~~ from control subjects, said control RNA having been detected in said samples from said control subjects, and said difference identifying said gene as a marker of said disease,

thereby identifying said two or more markers useful for diagnosing said disease.

55. (Currently amended) A method of identifying two or more markers useful for diagnosing a disease, said method comprising:

for each gene of a collection of two or more genes, wherein said gene is expressed in

blood and in a non-blood tissue of a subject not having said disease:

(a) producing amplification products from RNA of unfractionated cells of lysed blood samples from subjects having said disease, using primers specific only for RNA and/or cDNA complementary to said RNA, encoded by said gene of said subjects~~, wherein said gene is expressed in blood and in a non-blood tissue of a subject not having said disease~~;

(b) quantifying a level of said amplification products; and

(c) determining a difference between said ~~quantified~~ level of said amplification products and a quantified level of control amplification products produced ~~using said primers~~ from control RNA using primers specific only for said RNA, and/or cDNA complementary to said RNA, encoded by said gene, in RNA of unfractionated cells of lysed blood samples ~~which have not been fractionated into cell types,~~ from control subjects, said ~~control RNA~~ control amplification products having been detected in said samples from said control subjects~~,~~, wherein said difference identifies said gene as a marker of said disease, ~~.~~

thereby identifying two or more markers useful for diagnosing ~~the~~ said disease.

56. (new) The method of claim 19 or 55, wherein said quantifying of said level of said amplification products encoded by said gene in step (b) is effected by determining a quantity of said amplification products relative to a housekeeping gene.